Claims 1-11 stood rejected. The Applicants traverse all of the grounds of rejection raised by the Examiner. No claims have been objected to. In view of the foregoing amendments and the following response, the Applicants believe the amended and new claims presented herein are allowable. Reconsideration is respectfully requested.

SUPPORT

The claims have been amended to more clearly define the invention. Support for the amendments is either apparent, or is as described in the text below. Support for the claims as amended and the new claims may be found throughout the specification and in Figures 1 and 2. The text inserted into claims 1 and 7 finds support at the portion of the Glossary directed to "IDENTITY or SIMILARITY," and in the awareness of those of ordinary skill of the existence and availability of default parameters for the various computer algorithms that have been used to calculate sequence identity.

The identity formulation of claim 26 finds support, for example, in the text in the portion of the Glossary directed to "IDENTITY or SIMILARITY" which reads:

> In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences.

The identity formulation of claim 26 is the direct algebraic relationship implied by the above language. The above language, and the formulation, is free of any putative variation dependent upon the use of a given computer algorithm.

Claim 46 finds support, for example, at page 51, lines 19-31.

FORMAL DRAWINGS

Upon allowance, Applicants will provide formal drawings in the instant application incorporating the Examiner's suggestions at page 7, second paragraph of the Office Action.

RESTRICTION REQUIREMENT

The Applicants hereby affirm the provisional election of Group I (claims 1-11) with traverse made by the undersigned in a telephone conversation with the Examiner on December 3, 1997.

OBJECTION TO THE SPECIFICATION

At page 7, second paragraph of the Office Action the Examiner indicates that the specification has certain informalities. The Applicants are in the process of providing a new sequence listing which switches SEQ ID NOS: 1 for 2.[1] Support for this change may be found throughout the specification and in the figures. The Applicants have also amended the Brief Description of the Drawings. In view of these amendments the Applicants respectfully request that the Examiner remove the rejection to the specification.

CLAIM REJECTIONS UNDER 35 U.S.C. §112, FIRST PARAGRAPH

Claim 1-3 and 7-11 stood rejected under 35 U.S.C. §112, first paragraph for the reasons asserted in the Office Action. Applicant respectfully traverses.

In one aspect, the Office Action asserts:

> Since such a reference polynucleotide, e.g. a cloning vector comprising sequences consisting of the recited coding sequence, may encode the recited amino acid sequence while also comprising other unspecified polynucleotide sequences, the claimed polynucleotide need have no sequences corresponding to the region of the reference polynucleotide encoding the amino acid sequence, e.g. a cloning vector backbone. Therefore the open language of the claim can be interpreted to include any and all unspecified nucleotide sequences.

Applicant respectfully disagrees with this interpretation of the claims. However, in seeking to clearly obviate the rejection, the claims in question have been amended to recite "reference polynucleotide sequence consisting of a sequence encoding a polypeptide". This change seeks to

[1] Applicant's submission of the corrected Sequence Listing is delayed because it is seeking to submit the Sequence Listing in conformance with the revised Sequence Listing requirements. Nonetheless, this paper, Applicant respectfully submits, addresses all the substantive issues.

make it still more clear that the comparison is to exactly that sequence recited as the comparison sequence, such as in claim 1 that encoding amino acids 1 to 256 of SEQ ID NO:2.

The next portion of the rejection recites:

> In addition for claim 7, the recited deposited clone does not comprise a cDNA sequence according to the specification, but rather is the genomic source of the polynucleotide whose sequence is set forth as SEQ ID NO: 2 (see para. bridging pages 14-15). Consequently, the mature polypeptide recited in claim 7 could be interpreted to refer to any staphylococcal protein, not just the polypeptide whose sequence is set forth as SEQ ID NO: 1. The specification does not describe how to make and use any and all such unspecified sequences which the claims appear to embrace.

This aspect of the rejection is addressed, it is respectfully submitted, by the clarifying amendment replacing "cDNA" with "FabI gene."

Next, the Office Action posits, among other things:

> It is noted that over the coding region, the reference polynucleotides can have as little as 66% sequence identity with each other due to the degeneracy of codon sequences. Therefore a polynucleotide with as little as 70% sequence identity over a region corresponding to the coding region of the reference polynucleotide, can have as little as 46% (70% of 66%) nucleotide sequence identity with a natural *S. aureus* sequence encoding FAB I, such as that set forth as SEQ ID NO: 2. It is also noted that such a polynucleotide might encode a polypeptide with as little as 70% sequence identity to SEQ ID NO: 1, if the nucleotide differences lead to codons specific for different amino acids or introduce a stop codon. The specification teaches how to use the claimed polynucleotides to make FAB I polypeptides of fragments thereof for making antibodies and for screening assays for compounds that enhance or inhibit the function of FAB I or express a fragment or all of FAB I for therapeutic treatments, e.g. immunization, or to use as hybridization probes for sequences which have at least 95% sequence identity with the probe sequence, presumably natural sequences which encode FAB I or as PCR primers to amplify a natural sequence, such as might be used for a diagnostic assay for the presence of *S. aureus*.
>
> Regardless of the use of the polynucleotides, the uses taught in the specification require that either the nucleotide sequence or amino acid sequence be nearly identical to a natural nucleotide or amino acid sequence of an FAB I protein, mostly the *S. aureus* FAB I given that the claim are limited to the *S. aureus* FAB I sequence as the amino acid sequence encoded by the reference nucleic acid. Where the use requires polynucleotides encoding an active FAB I protein, it is known in the art that even conservative amino acid substitutions can adversely affect proper folding and biological activity if amino acids that are critical for such functions are substituted, and the relationship between the sequence of a polypeptide and its tertiary structure is neither well understood nor predictable (see Ngo, pp. 433 and

> 492-495). The specification contains no guidance or citations of relevant prior art that would inform the skilled artisan of which amino acid residues of SEQ ID NO: I could be altered without adversely affecting its folding or its biological activity. For polynucleotides encoding a FAB I polypeptide, or fragment thereof for inducing an immunological response, such as for the production of antibodies or for immunization, the specification does not teach which fragments of the natural FAB I protein might be sufficiently antigenic or immunogenic for such purposes, but more to the point, how such peptides could be altered by substituting, inserting or deleting amino acids to retain or improve the antigenic or immunogenic properties of the peptide.

The Applicant respectfully points out that the specification is replete with teachings enabling a person skilled in the art to which the invention pertains, or with which it is most nearly connected, to make or use the invention commensurate with the scope of these claims.

For example, in the "Polypeptides" portion of the Glossary and in the "Polypeptides" Section, the Applicant teaches how to obtain such sequences when they state:

> It will be appreciated that polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally occurring amino acids, and that many amino acids, including the terminal amino acids, may be modified in a given polypeptide, either by natural processes, such as processing and other post-translational modifications, but also by chemical modification techniques which are well known to the art. Even the common modifications that occur naturally in polypeptides are too numerous to list exhaustively here, but they are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art.
>
> Among the known modifications which may be present in polypeptides of the present are, to name an illustrative few, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.
>
> Such modifications are well known to those of skill and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as, for instance *PROTEINS - STRUCTURE AND MOLECULAR*

PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as, for example, those provided by Wold, F., Posttranslational Protein Modifications: Perspectives and Prospects, pgs. 1-12 in *POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter et al., (1990) *Meth. Enzymol. 182*:626-646 and Rattan et al., (1992) *Protein Synthesis: Posttranslational Modifications and Aging*, Ann. N.Y. Acad. Sci. 663: 48-62.

It will be appreciated, as is well known and as noted above, that polypeptides are not always entirely linear. For instance, polypeptides may be branched as a result of ubiquitination, and they may be circular, with or without branching, generally as a result of posttranslation events, including natural processing event and events brought about by human manipulation which do not occur naturally. Circular, branched and branched circular polypeptides may be synthesized by non-translation natural process and by entirely synthetic methods, as well.

Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. In fact, blockage of the amino or carboxyl group in a polypeptide, or both, by a covalent modification, is common in naturally occurring and synthetic polypeptides and such modifications may be present in polypeptides of the present invention, as well. For instance, the amino terminal residue of polypeptides made in *E. coli* or other cells, prior to proteolytic processing, almost invariably will be N-formylmethionine. During post-translational modification of the peptide, a methionine residue at the NH_2-terminus may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of the protein of the invention.

The modifications that occur in a polypeptide often will be a function of how it is made. For polypeptides made by expressing a cloned gene in a host, for instance, the nature and extent of the modifications in large part will be determined by the host cell posttranslational modification capacity and the modification signals present in the polypeptide amino acid sequence. For instance, as is well known, glycosylation often does not occur in bacterial hosts such as, for example, *E. coli*. Accordingly, when glycosylation is desired, a polypeptide should be expressed in a glycosylating host, generally a eukaryotic cell.

It will be appreciated that the same type of modification may be present in the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications.

In general, as used herein, the term polypeptide encompasses all such modifications, particularly those that are present in polypeptides synthesized by expressing a polynucleotide in a host cell.

* * * * *

The invention also relates to fragments, analogs and derivatives of these polypeptides. The terms "fragment," "derivative" and "analog" when referring to the polypeptide of Figure 1

[SEQ ID NO:2], means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analog includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide. In certain preferred embodiments it is a recombinant polypeptide.

The fragment, derivative or analog of the polypeptide of Figure 1 [SEQ ID NO:2] may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Among the particularly preferred embodiments of the invention in this regard are polypeptides having the amino acid sequence of FAB I set out in Figure 1 [SEQ ID NO:2] variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of the fragments. Alternatively, particularly preferred embodiments of the invention in this regard are polypeptides having the amino acid sequence of the FAB I, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of the fragments.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

Further particularly preferred in this regard are variants, analogs, derivatives and fragments, and variants, analogs and derivatives of the fragments, having the amino acid sequence of the FAB I polypeptide of Figure 1 [SEQ ID NO:2] in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the FAB I. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polypeptides having the amino acid sequence of Figure 1 [SEQ ID NO:2] without substitutions.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The polypeptides of the present invention include the polypeptide of SEQ ID NO:2 (in particular the mature polypeptide) as well as polypeptides which have at least 80% identity to the polypeptide of SEQ ID NO:2 and more preferably at least 90% similarity (more preferably at least 90% identity) to the polypeptide of SEQ ID NO:2 and still more preferably at least 95% similarity (still more preferably at least 95% identity) to the polypeptide of SEQ ID NO:2 and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 30 amino acids and more preferably at least 50 amino acids.

> Fragments or portions of the polypeptides of the present invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, the fragments may be employed as intermediates for producing the full-length polypeptides. Fragments or portions of the polynucleotides of the present invention may be used to synthesize full-length polynucleotides of the present invention.

The Office Action points out that the rules for protein folding are not well understood, from which it posits that undue experimentation would be required to arrive at other FabI polypeptides. Granted that Applicant may not know the *tertiary* structure of FabI, but Applicant does have a reasonable basis to infer at least some of the biology of the protein that Applicant has identified. See, pages 1-3 of the application. Like many other inventors of chemical inventions, Applicant may not have knowledge of tertiary structure; but Applicant does possess the primary structure of a material which will fold to an appropriate tertiary structure. Applicant does not need to know tertiary structure, as he can make the easier determination of whether a polypeptide has function.

The Office Action cites *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 927 F.2d 1200, 18 USPQ2d 1016 (Fed. Cir. 1991) in support of the rejection for asserted lack of enablement. Applicant first notes that its claims are nothing like the claims at issue in *Amgen* which recited "sufficiently duplicative of that of erythropoietin to allow possession of the biological property of causing bone marrow cells to ..." Applicants claims are founded on a concrete boundary of relatedness to certain reference sequences, while the claims at issue in Amgen were without practical boundaries. Second, Applicants note that enablement rests on what is "undue" experimentation at the time of filing, and this measure clearly changes with developments in automation, standardization, credible and reproducible supplies, methodologies, and the like. Much prospective experimentation which was "undue" in the 1980s when the patent at issue in *Amgen* was filed is no longer undue experimentation.

Further, Applicant respectfully notes that the hybridization uses of the invention are not limited to "stringent condition" hybridizations, and that use of the invention to uncover highly related sequences within other isolates of *Staphylococcus* is a readily apparent use of the invention.

Further, the Applicant respectfully submits that to satisfy the "how to make" requirement of 35 USC 112 one need only show how to make each embodiment claimed. The Applicant need not show that each and every embodiment can be made in any specified period of time or that all or a substantial portion of the embodiments have been made.

In light of these amendments and remarks, Applicant respectfully submits that the rejection under 35 U.S.C. §112, First Paragraph should be withdrawn.

35 U.S.C. §112, SECOND PARAGRAPH

Claims 1-11 stood rejected under 35 U.S.C. §112, Second Paragraph. This rejection is respectfully traversed.

In one aspect, the rejection asserts that the meaning of percent identity is not well enough established in the claims. The Applicant respectfully disagrees and submits that the term "identity" has a meaning well known to those of skill in the art. Moreover, the Applicant has recited a number of algorithms which are provided on the GCG program package with default parameters. These algorithms include, for example, BLASTP, BLASTN and FASTA. The definition of "Identity" set forth at pages 8-9 of the specification references the GCG program.

Further, one skilled in the art would know that gap penalty parameters become useful for determining sequence alignments of sequences below about 60-70% identity as compared to a reference or query sequence. One skilled in the art would also know that for identity values above about 70% identity, as compared to a reference or query sequence, the gap penalty parameters become less of an important factor in determining the alignment of any two sequences. Moreover, the Applicant teaches, the portion of the Glossary directed to "IDENTITY or SIMILARITY," that preferred methods to determine identity are designed to give the largest match between the sequences tested. This teaching clearly indicates to those skilled in the art that even given the dependency of the algorithm result on the specific algorithm suggested by the Examiner, it is a trivial exercise to select which result falls within the scope of the claims, viz, the one that gives the largest match between the sequences tested.

Solely to facilitate prosecution, and in no way acquiescing to the Examiner's rejection, the Applicant has amended the claims to clarify the scope of the claims which Applicant

believes overcomes the Examiner's concerns under §112, first and second paragraphs regarding the algorithm to determine percent identity. In one of the claims (claim 26), an algebraic formula is recited based on the support referenced in the text above.

The rejections set forth on pages 13 and 14 of the Office Action, particularly with reference to claims 4-7, 10 and 11, have been addressed by the clarifying amendments submitted herewith, and by the revised Sequence Listing that is to be submitted.

In light of these amendments and remarks, Applicant respectfully submits that the rejection under 35 U.S.C. §112, Second Paragraph should be withdrawn.

35 U.S.C. §102

The rejection under 35 U.S.C. §102(b) is, it is respectfully submitted, no longer applicable in light of the clarifying amendments submitted herewith.

35 U.S.C. §101

Without conceding the validity of the asserted interpretation of 35 U.S.C. §101, Applicant respectfully submits that the amendments render the rejection asserted under this statute no longer applicable.

The Applicants have canceled claims without prejudice or disclaimer of the subject matter therein. Moreover, the Applicants reserve the right to prosecute, in one or more patent applications, the canceled claims, the claims to non-elected inventions, the claims as originally filed, and any other claims supported by the specification. Any amendments made herein to the claims were made to solely expedite or otherwise facilitate prosecution and were not made nor should they be construed to have been made to overcome any issue of unpatentability of the claims as they existed prior to such amendments, or in any way to limit the scope of equivalents.

Serial No.:08/790,043
Group Art Unit No.: 1819

The Applicants thank the Examiner for the Office Action and believe this response to be a full and complete response to such Office Action. Accordingly, favorable reconsideration of the application and allowance of the pending and new claims is earnestly solicited.

Respectfully submitted,

Date: June 23, 1998

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